

Sequence Listing.ST25.txt SEQUENCE LISTING

<110>	GTC Biotherapeutics, Inc. Edge, Michael D Pollock, Daniel Echelard, Yann Meade, Harry M Rybak, Susanna M						
<120>	0> Transgenically Produced Fusion Proteins						
<130>	> GTC-42D						
<140> <141>	us 10/608,710 2003-06-27						
<150> <151>							
<160>	<160> 11						
<170>	> PatentIn version 3.2						
<210> <211> <212> <213>	1 705 DNA Artificial						
<220> <223>							
<400> atggat	1 tttc aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcc	60					
cgcggc	gaca tccagatgac ccagagccca agcagcctga gcgctagcgt gggtgacaga	120					
gtgacc	atca cgtgtagtgc cagctcaagt gtaacttaca tgcactggta ccagcagaag	180					
ccaggt	aagg ctccaaagct gctgatctac agcacatcca acctggcttc tggtgtgcca	240					
agcaga	ttct ccggaagcgg tagcggcacc gactacacct tcaccatcag cagcctccag	300					
ccagag	gata tcgccaccta ctactgccag cagaggagta cttacccgct cacgttcggc	360					
caaggg	acca agctcgagat caaacggact gtggctgcac catctgtctt catcttcccg	420					
ccatct	gatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc	480					
tatccc	agag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc	540					
caggag	agtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg	600					
acgctg	agca aagcagacta cgagaaacac aaagtctacg cctgcgaagt cacccatcag	660					
ggcctg	agtt cgcccgtcac aaagagcttc aacaggggag agtgt	705					
<210> <211>	2 235						

<212> PRT <213> Artificial

<220>

<223> complete humanised light chain sequence

<400> 2

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Val Ile Met Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser 20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser 35 40 45

Ser Ser Val Thr Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala 50 60

Pro Lys Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro 65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile 85 90 95

Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg 100 105 110

Ser Thr Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys 115 120 125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu 130 135 140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe 145 150 155 160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
165 170 175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser 180 185 190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu 195 200 205

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser 210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 235

3

<210>

1870 DNA Artificial <220> expected PCR insert <223> <400> 3 aagcttgccg ccaccatgaa gttgtggctg aactggattt tccttgtaac acttttaaat 60 120 ggaattcagt gtgaggtgca gctgcagcag agcggtccag gtctcgtacg gcctagccag accetgagee teaegtgeac egeatetgge tteaacatta aggacaatta catgeactgg 180 240 300 gacactgagt acgcacctaa gtttcgcggc cgcgtgacaa tgctggcaga cactagtaag aaccagttca gcctgagact cagcagcgtg acagccgccg acaccgcggt ctattattgt 360 420 cacqtcctga tatacqccgg gtatctggca atggactact ggggccaagg gaccctcgtc 480 accgtgagct cggctagcac caagggccca tcggtcttcc ccctggcgcc ctgctccagg agcacctctg ggggcacagc ggccctgggc tgcctggtca aggactactt ccccgaaccg 540 600 gtgacggtgt cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg 660 ggcacccaga cctacacctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 720 780 agagtggagc tgaaaacccc actcggtgac acaactcaca cgtgccctag gtgtcctgaa 840 cctaaatctt gtgacacacc tcccccgtgc ccacggtgcc cagagcccaa atcttgcgac acgccccac cgtgtcccag atgtcctgaa ccaaagagct gtgacactcc accgccctgc 900 960 ccgaggtgcc cagcacctga actcctggga ggagcaacag gacacagtta tgagaagtac aacaagtggg aaacgataga ggcttggact caacaagtcg ccactgagaa tccagccctc 1020 1080 atctctcgca gtgttatcgg aaccacattt gagggacgcg ctatttacct cctgaaggtt 1140 ggcaaagctg gacaaaataa gcctgccatt ttcatggact gtggtttcca tgccagagag 1200 tggatttctc ctgcattctg ccagtggttt gtaagagagg ctgttcgtac ctatggacgt 1260 gagatccaag tgacagagct tctcgacaag ttagactttt atgtcctgcc tgtgctcaat attgatggct acatctacac ctggaccaag agccgatttt ggagaaagac tcgctccacc 1320 1380 catactggat ctagctgcat tggcacagac cccaacagaa attttgatgc tggttggtgt gaaattggag cctctcgaaa cccctgtgat gaaacttact gtggacctgc cgcagagtct 1440 gaaaaggaga ccaaggccct ggctgatttc atccgcaaca aactctcttc catcaaggca 1500 1560 tatctgacaa tccactcgta ctcccaaatg atgatctacc cttactcata tgcttacaaa 1620 ctcggtgaga acaatgctga gttgaatgcc ctggctaaag ctactgtgaa agaacttgcc Page 3

tcactgcacg	gcaccaagta	cacatatggc	ccgggagcta	caacaatcta	tccttctgct	1680
gggacttcta	aagactgggc	ttatgaccaa	ggaatcagat	attccttcac	ctttgaactt	1740
cgagatacag	gcagatatgg	ctttctcctt	ccagaatccc	agatccgggc	tacctgcgag	1800
gagaccttcc	tggcaatcaa	gtatgttgcc	agctacgtcc	tggaacacct	gtactaataa	1860
tctagagaga						1870

- <210> 4
- <211> 613
- <212> PRT
- <213> Artificial
- <220>
- <223> humanised Fd mutant HCPB sequence
- <400> 4

Met Lys Leu Trp Leu Asn Trp Ile Phe Leu Val Thr Leu Leu Asn Gly 1 10 15

Ile Gln Cys Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg 20 25 30

Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile 35 40 45

Lys Asp Asn Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu 50 60

Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala 75 80

Pro Lys Phe Arg Gly Arg Val Thr Met Leu Ala Asp Thr Ser Lys Asn $85 \hspace{1.5cm} 90 \hspace{1.5cm} 95$

Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val 100 105 110

Tyr Tyr Cys His Val Leu Ile Tyr Ala Gly Tyr Leu Ala Met Asp Tyr 115 120 125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly 130 140

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Gly Gly 145 150 155 160

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Page 4 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe 180 185 190 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val 195 200 205 Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val 210 215 220 Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Leu Lys 235 230 235 Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys Pro Glu Pro 245 250 255 Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys 260 265 270 Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser 275 280 285 Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu 290 300 Gly Gly Ala Thr Gly His Ser Tyr Glu Lys Tyr Asn Lys Trp Glu Thr 305 310 315 320 Ile Glu Ala Trp Thr Gln Gln Val Ala Thr Glu Asn Pro Ala Leu Ile 325 330 335 Ser Arg Ser Val Ile Gly Thr Thr Phe Glu Gly Arg Ala Ile Tyr Leu 340 345 350 Leu Lys Val Gly Lys Ala Gly Gln Asn Lys Pro Ala Ile Phe Met Asp 355 360 365 Cys Gly Phe His Ala Arg Glu Trp Ile Ser Pro Ala Phe Cys Gln Trp 370 380 Phe Val Arg Glu Ala Val Arg Thr Tyr Gly Arg Glu Ile Gln Val Thr 385 390 395 400 Glu Leu Leu Asp Lys Leu Asp Phe Tyr Val Leu Pro Val Leu Asn Ile 405 410 415 Sequence Listing.ST25.txt
Asp Gly Tyr Ile Tyr Thr Trp Thr Lys Ser Arg Phe Trp Arg Lys Thr
420 425 430

Arg Ser Thr His Thr Gly Ser Ser Cys Ile Gly Thr Asp Pro Asn Arg $435 \hspace{1.5cm} 440 \hspace{1.5cm} 445$

Asn Phe Asp Ala Gly Trp Cys Glu Ile Gly Ala Ser Arg Asn Pro Cys 450 455 460

Asp Glu Thr Tyr Cys Gly Pro Ala Ala Glu Ser Glu Lys Glu Thr Lys 465 470 475 480

Ala Leu Ala Asp Phe Ile Arg Asn Lys Leu Ser Ser Ile Lys Ala Tyr 485 490 495

Leu Thr Ile His Ser Tyr Ser Gln Met Met Ile Tyr Pro Tyr Ser Tyr 500 505 510

Ala Tyr Lys Leu Gly Glu Asn Asn Ala Glu Leu Asn Ala Leu Ala Lys 515 520 525

Ala Thr Val Lys Glu Leu Ala Ser Leu His Gly Thr Lys Tyr Thr Tyr 530 540

Gly Pro Gly Ala Thr Thr Ile Tyr Pro Ser Ala Gly Thr Ser Lys Asp 545 550 555 560

Trp Ala Tyr Asp Gln Gly Ile Arg Tyr Ser Phe Thr Phe Glu Leu Arg 565 570 575

Asp Thr Gly Arg Tyr Gly Phe Leu Leu Pro Glu Ser Gln Ile Arg Ala 580 585 590

Thr Cys Glu Glu Thr Phe Leu Ala Ile Lys Tyr Val Ala Ser Tyr Val
595 600 605

Leu Glu His Leu Tyr 610

<210> 5

<211> 96 <212> PRT

<213> Artificial

<220>

<223> preproHCPB with C-terminal Leu

<400> 5

His His Gly Glu His Phe Glu Gly Glu Lys Val Phe Arg Val Asn Page 6 5

Val Glu Asp Glu Asn His Ile Asn Ile Ile Arg Glu Leu Ala Ser Thr 20 25 30

Thr Gln Ile Asp Phe Trp Lys Pro Asp Ser Val Thr Gln Ile Lys Pro 35 40 45

His Ser Thr Val Asp Phe Arg Val Lys Ala Glu Asp Thr Val Thr Val 50 55 60

Glu Asn Val Leu Lys Gln Asn Glu Leu Gln Tyr Lys Val Leu Ile Ser 70 75 80

Asn Leu Arg Asn Val Val Glu Ala Gln Phe Asp Ser Arg Val Arg Leu 85 90 95

<210> 6

<211> 40

<212> PRT

<213> peptide linker

<400> 6

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser 1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly 20 25 30

Gly Gly Gly Ser Gly Gly Gly 40

<210> 7

<211> 11

<212> PRT

<213> peptide linker

<400> 7

Gly Gly Gly Ser Gly Gly Gly Gly Ser 1 5 10

<210> 8

<211> 20

<212> PRT

<213> peptide linker

<400> 8

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser 10 15

```
Gly Gly Gly 20
<210>
<211> 17
<212> PRT
      17
<213>
      peptide linker
<400> 9
Ser Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser 10 15
Pro
<210>
       10
<211>
       20
<212> DNA
<213> nucleic acid primer
<400> 10
                                                                        20
tgtgctcctc tccatgctgg
<210>
       11
       20
<211>
<212> DNA
<213> nucleic acid primer
<400> 11
                                                                        20
tggtctgggg tgacacatgt
```